ATGGATTTCGGACTGGCCCTCCTGCTGGCGGGGCTTCTGGGGCTCCTCCTCGGCCAGTCCCTCCAGGTGAAGCCCCTGCA H D F G L A L L L A G L L G L L G O S L O V K P L O	80
GGTGGAGCCCCGGAGCCGGTGGCCGTGGCCTTGGGCGCCTCGCGCCAGCTCACCTGCCGCCTGGCCTGCGCGGACC V E P P E P V V A V A L G A S R Q L T C R L A C A D	160
GCGGGGCCTCGGTGCAGTGGCGGGGCCTGGACACCAGCCTGGGCGCGGTGCAGTCGGACACGGGCCGCAGCGTCCTCACC R G A S V O W R G L D T S L G A V O S D T G R S V L T	240
GTGCGCAACGCCTCGCTGTCGGCGGCGGGGACCCGCGTGTGCGTGGGCTCCTGCGGGGGCCGCACCTTCCAGCACACCGT V R N A S L S A A G T R V C V G S C G G R T F O H T V	320
GCAGCTCCTTGTGTACGCCTTCCCGGACCAGCTGACCGTCTCCCCAGCAGCCCTGGTGCCTGGTGACCCGGAGGTGGCCT D L V Y A F P D Q L T V S P A A L V P G D P E V A	400
GTACGGCCCACAAAGTCACGCCCGTGGACCCCAACGCGCTCTCCTTCTCCCTGCTCGTCGGGGGCCAGGAACTGGAGGGG T A H K V T P V D P N A L S F S L L V G G Q E L E G	480
GCGCAAGCCCTGGGCCGGAGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGACGTGCTGTTCAGGGTGACAGA A O A L G P E V O E E E E P O G D E D V L F R V T E	560
GCGCTGGCGGCCCCTGGGGACCCCTGTCCCGCCCGCCCTCTACTGCCAGGCCACGATGAGGCTGCCTGGCTTGG	640
ASCTCASCCACCSCCATCCCCGTCCTGCACAGCCCGACCTCCCCGGAGCCTCCCCGACACCACCACCACCACCTCCCCGGAGCCT	7 20
CCCAACACCACCTCCCCGGAGTCTCCCGACACCACCTCCCGGAGTCTCCCGACACCACCTCCCAGGAGGCTCCCGACACC	800
CACCTCCCAGGAGCCTCCCGACACCACCTCCCAGGAGCCTCCCGGACACCCTCCCGGAGCCTCCCGACAAGACCTCCCCAAGACACACCACCACCACCACCACCACCACCACCAC	880
CGGAGCCGCCCCCAGCAGGGCTCCACACACCCCCAGGAGCCCAGGGCTCCACCAGGACTCGCCCCTGAGATCTCC	960
CASSCTGSSCCCAGGGGGGGGGGGGGGGGGGGGGGGGGGG	1040
GACCAGGAGTGCGGGACTGCTGCTGCTGCTGCCCACGTATCACCTCTGGAAACGCTGCCGGCACCTGGCTG T S S A V L G L L L A L P T Y H L W K R C R H L A	1120
ASSACSACACCACCACCACCAGCTTCTCTGAGGCTTCTGCCCCAGGTGTCGGCCTGGGCTGGGTTAAGGGGGACCGGCCAG	1200
CTCGGGATCASCCCTCCTGAGTGGCCAGCCTTTCCCCCCTGTGAAAGCAAAATAGCTTGGACCCCTTCAAGTTGAGAACT V G L S P S	1280
G3TCA3G3CAAACCTGCCTCCCATTCTACTCAAAGTCATCCCTCTGCTCACAGAGATGGATG	1360
TTGGAGAAGCTCATCAGAAACTCAAAAAGAAGGCCACTGTTTGTCTCACCTACCCATGACCTGAAGCCCCTCCCT	1440
TCCCCACCTTTCTGGACGGAACCACGTACTTTTTACATACA	1520
CAASSTGTGSSSTGASCACCCTGGGCCCCTGTCGTCAGGACCTCCTGAGGCTTTGGCAAATAAACCTCCTAAAATGATAA	1600
A1411A1A1A1A1AAAAAAAAA 1624	

FIGURE 1

ATGGATTTCGGACTGGCCCTCCTGCTGGCGGGGCTCTCTGGGGCTCCTCCGGCCAGTCCCTCCAGGTGAAGCCCCTGCA 8C)
GGTGGAGCCCCGGAGCCGGTGGCCGTGGCCTTGGGCGCCTGGCCTGCGCGGACC 16	50
GCGGGGCCTCGGTGCAGTGGCGGGGCCTGGACACCAGCCTGGGCGGGGGGGG	Ю
GTGCGCAACGCCTCGCTGTCGGCGGCCGGGGCCGGGCCG	!O
GCAGCTCCTTGTGTACGCCTTCCCGGACCAGCTGACCGTCTCCCCAGCAGCCCTGGTGCCTGGTGACCCGGAGGTGGCCT 40	0
GTACGGCCCACAAAGTCACGCCCGTGGACCCCAACGCGCTCTCCTTCTCCCTGCTCGTCGGGGGCCAGGAACTGGAGGGG 48	0
GCGCAAGCCCTGGGCCCGGAGGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGACGTGCTGTTCAGGGTGACAGA 56 A C A L G P E V Q E E E E P Q G D E D V L F R V T E	0
GCGCTGGCGGCTGCCGCCCTGGGGACCCCTGTCCCGCCCG	0
ASCICAGCCACCGCCAGGCCATCCCCGTCCTGCACAGCCTCCCGGAGCCTCCCGGAGCCTCCCGGAGCCTCCCGGAGTCT 720	S
CCCGACACCACCTCCCGGAGTCTCCCGACACCACCTCCCGAGGGCCTCCCGGAGGCCTCCCGGAGGCCTCCCGACAA 800	5
GACCTCCCCGGAGCCCGCCCCAGCAGGGCTCCACCACACCCCCCAGGAGCCCAGGGCTCCACCAGGACTCGCCGCCCTG 880	2
AGATETECEAGGETGGGECCACGCAGGGAGAAGTGATCCCAACAGGCTCGTCCAAACCTGCGGGTGACCAGCTGCCCGCG 960	כ
GCTCTGTGGACCAGCAGTGCGGGACTGCTGCTGCTGCCTGC	1 0
CCTGGCTGAGGACGACCCACCACCAGCTTCTCTGAGGCTTCTGCCCCAGGTGTCGGCCTGGGCTGAGGTTAAGGGGGA 112 L A E D D T H P P A S L R L L P O V S A W A G L R G	20
CCGGCCAGGTCGGGATCAGCCCCTCCTGAGTGGCCAGCCTTTCCCCCCTGTGAAAGCAAAATAGCTTGGACCCCTTCAAGT 120	00
TGAGAACTGGTCAGGGCAAACCTGCCTCCCATTCTACTCAAAGTCATCCCTCTGTTCACAGAGATGGATG	30
TIGCCICITIGGAGAAGCICATCAGAAACTCAAAAGAAGGCCACIGTITGTCTCACCTACCCATGACCTGAAGCCCCTCC 136	30
CTGAGTGGTCCCCACCTTTCTGGACGGAACCACGTACTTTTTACATACA	0
CGTAAGACCAAGCTGTGCCCTGACCACCCTGGGCCCCTGTCGTCAGGACCTCCTGAGGCTTTGGCAAATAAACCTCCTAA 152	0:
AATGAAAAAAAAAAAA 1539	

FIGURE 2

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3/20 Figure 3

M D R G L A L L <u>A G</u> L L C L L <u>O P G C</u> G O S L Q Y GAAGCCCCTGCAGCTGGAGCCCCGGAGCCGGTGGTGGTGGCCGTGGCCCTCTCGCCAGCTCACCTTGCCCCTGG 180 K P L O V E P P F P V V A V A L G A S R O L 1 C R L DCADRGATYCWRGLDTSLGAYOSDAGR AGCGTCCTCACCGTGCGCAACGECTCGCTGTCGGCGGGCCGGGACCCGTGTGTGCGTGGGCTCCTRCGGGGGCCGCACCTT 320 S V L T V R N A S L S A A G T R V C Y G S C G G R T F CCAGCACACCGTGCGGCTCCTTGTGTACGCCTTCCCGGACCACCTGACCATCTCCCCGGCAGCCCTGGTGCCTGGTGACC 400 O H T Y R L L Y Y A F P O O L T I S P A A L Y P G D CGGAGGTGGCC1GTACGGCCAAAAAGTCACGCCTGTGGACCCCAATGCGCTCTCCTTCTCCTGCTGCTCCTGGGGGACCAC 480 LE V A C T A H K V T P V D P N A L S F S L I. L G D O C L C A O A L G P E V E F C C C C P O È E E D V L F CAGGGTGACAGAGGGCTGGCGGGCTGCCCACCCTGGGCAACCCCTGTCCTGGCGGGGCTCTACTGCCAGGCCACGATGAGGG 640 RVTERWRLPTLATPVIPALYCOATMR L P G L E L S H R D A I P V L II G P T S R E P P D T T S P E P R A A T S P E T T P Q C G S T H S P R S P G S TRICRPEIS DAGPIDGEVIPIGS SKP T C C C L P A A L W T S S A V L C L L L A L P T Y H CTCTGSAAAGGTTGCCGGCACCTGGCTGAGGGGGGGCGCCCACCGAGCTTUTCTGAGTAGCCAGGCTTCCCCCCTGTR 1040 L W K P C R H L A E D G A H P F A S L S S C P F P L . ANDGGAAAATAGGTTGGACCCCTTCAAGCTGAGAAC136°CCGGGCAAACCTGCCTGCCATTCTATTCAAACTCATCCC1 1120 CATATATTGATTCATGTGTCATATCTCCCTAAAATGTGTAAAACCAGCTGTGCCCCGACCATGTGTGGCCCCTGCCATCA 1360 SBACCTCCTGAEGCTTTGGCAAATAAACETCCTAAAAGGATAGAAACTGAAACTTGTCGCCGCGCGCGGGTGGCTCAAGCC 1440 TGTANTCCCAGCACTTTRGGAGGCCGAGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGGAGACCCGTGGCTAACCCGTGAA 1520

Figure 4a

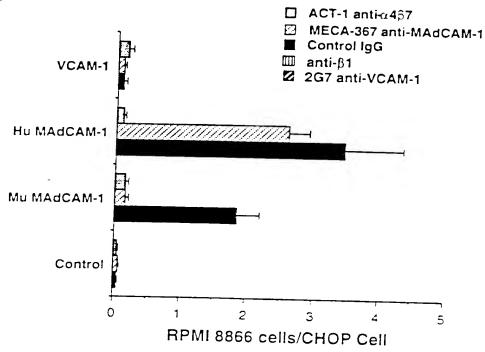
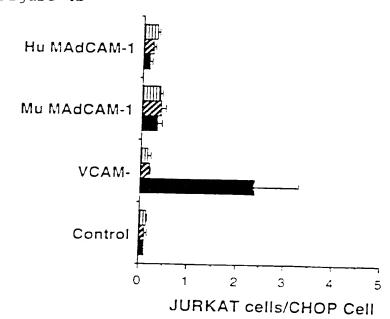


Figure 4b



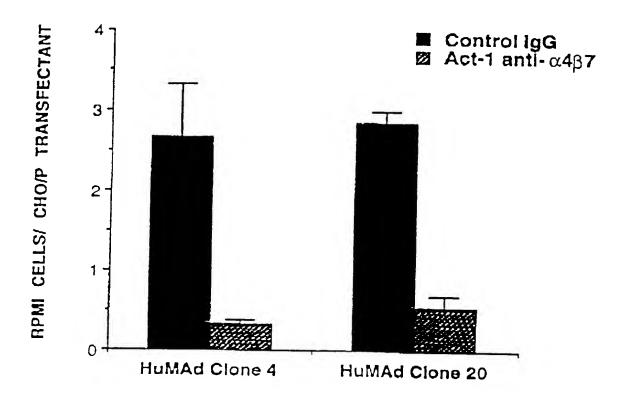


FIGURE 5

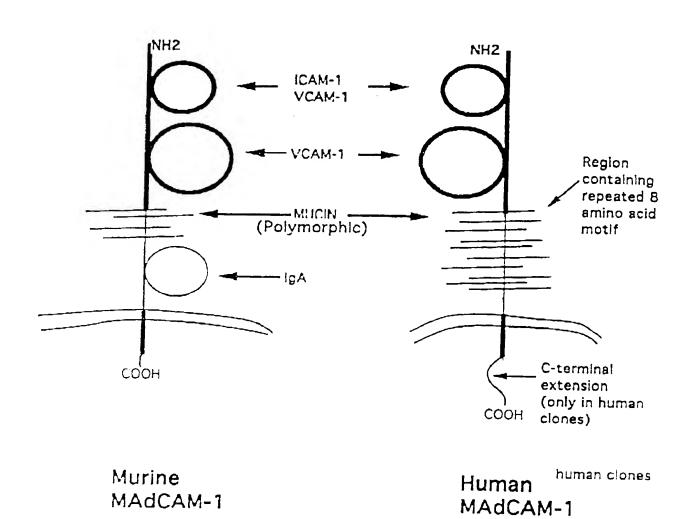
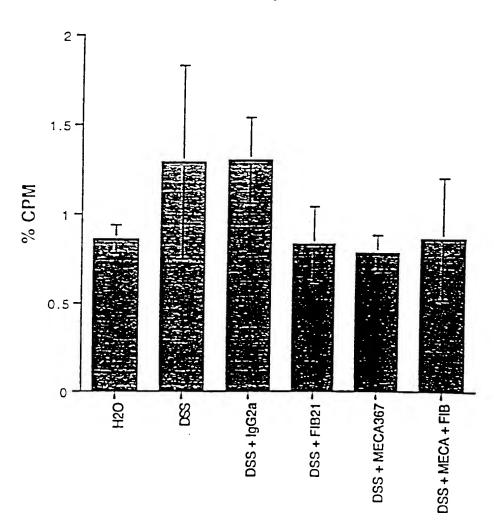


Figure 6

PCT/US96/02153 7/20 Rat IgG2a FIB-30 F1B-21 Ø :0; STRUCTURAL DAMAGE ASCENDING COLON FIGURE 7B TISSUE DESCENDING 2.5 0.5-.5-**EYCOS** Rat IgG2a F1B-30 F1B-21 \mathbf{Z} 至 ASCENDING COLON TISSUE FIGURE 7A DESCENDING COLON 2.5-0.5 1.5-**3000**

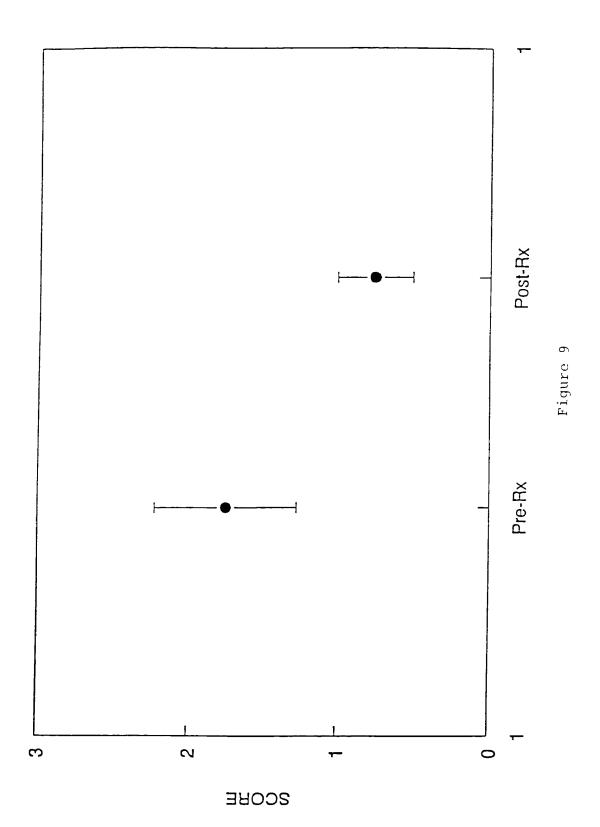
INFLAMMATION

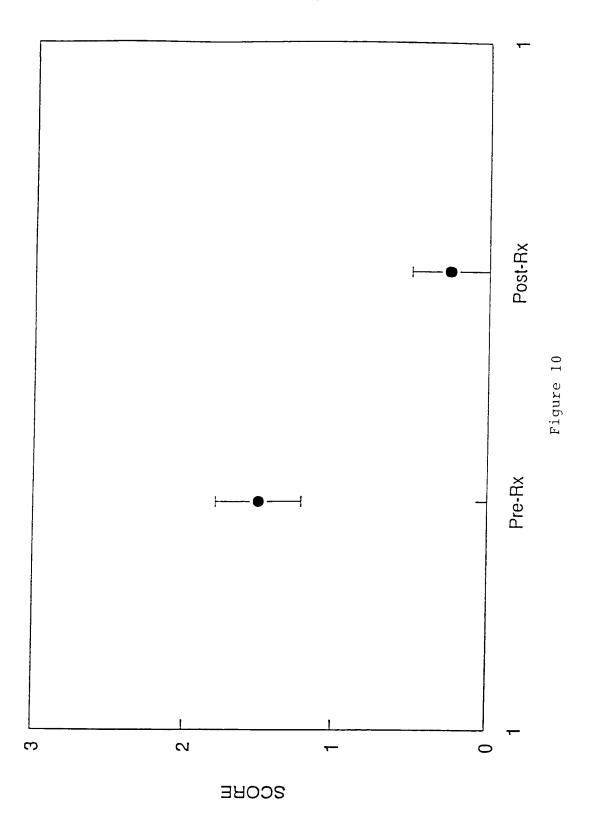
Figure 8



TREATMENT







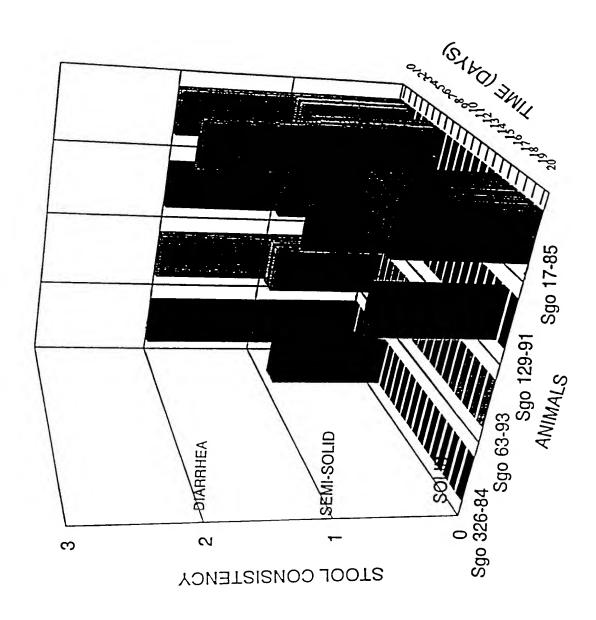


Figure 11

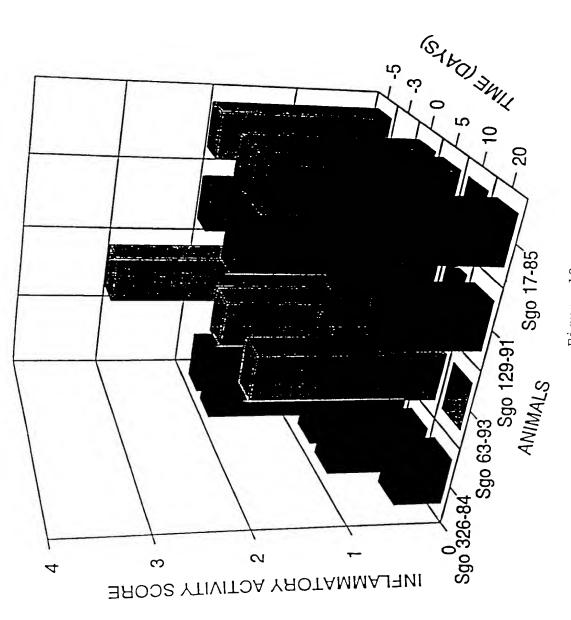
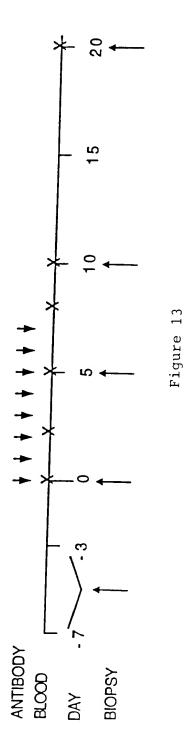


Figure 12



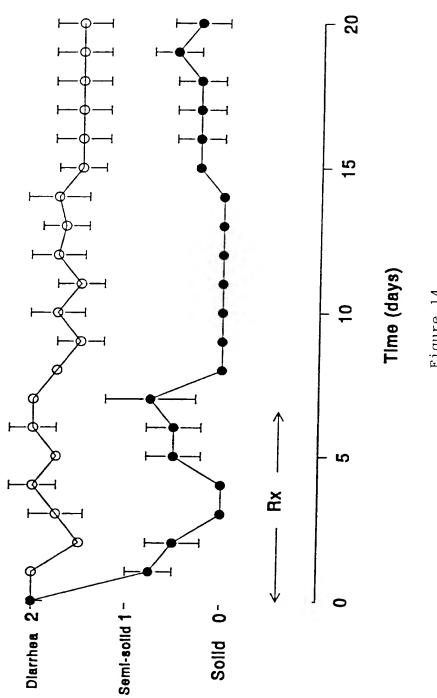
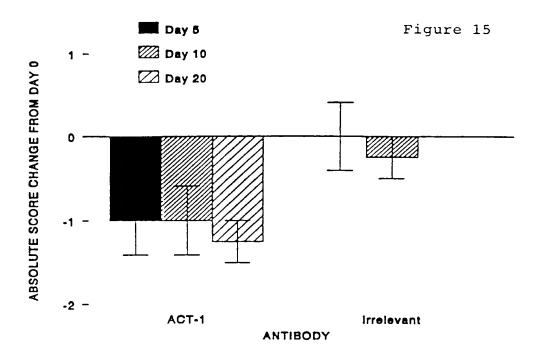
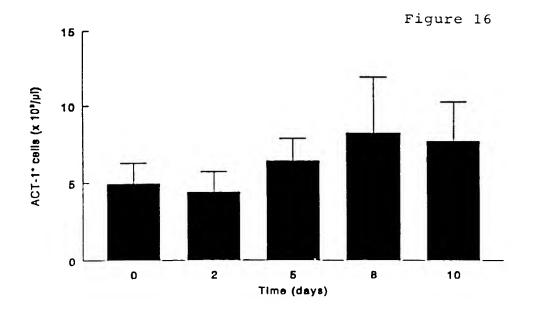
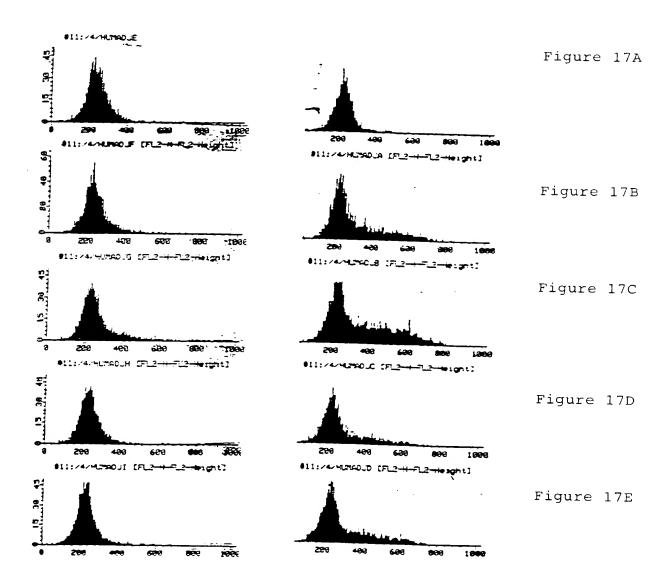


Figure 14







PCT/US96/02153

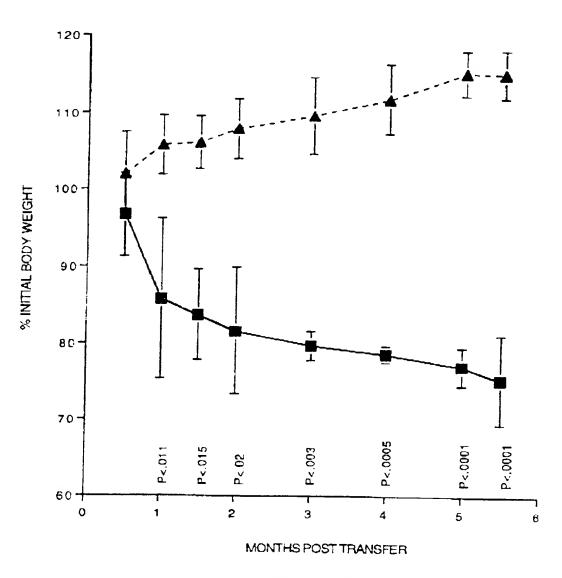
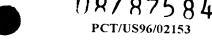


Figure 18



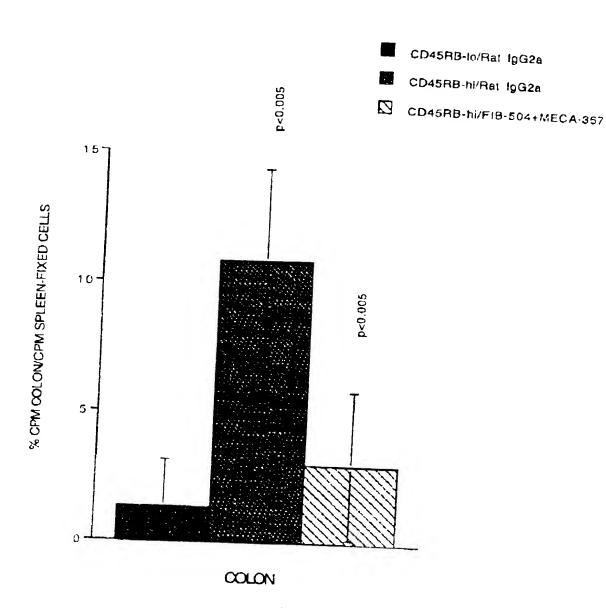


Figure 19

Figure 20

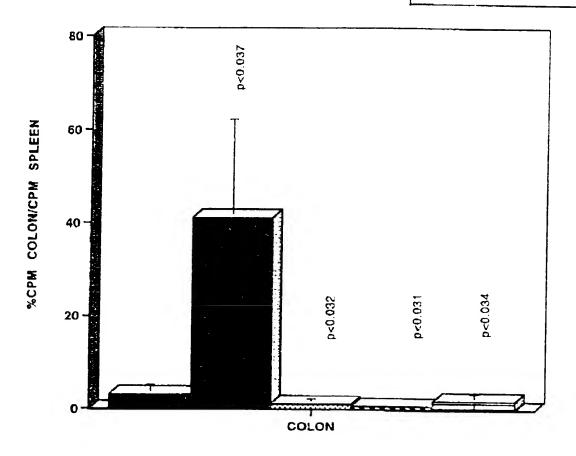
CD45RBlo/Rat 1gG2a

CD45RBhi/Rat IgG2a

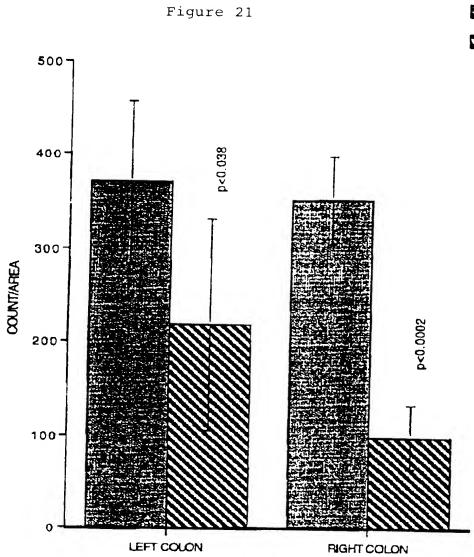
™ CD45RBhi/F1B-504

CD45RBhi/MECA-367

CD45RBhi/FIB504+MECA367







Rat IgG2a

FIB504 + MECA387